CORRECTED SEQUENCE LISTING

<110> Cahoon, Rebecca
        Gutteridge, Steven
        Lee, Jian-Ming
        McGonigle, Brian
        Rafalski, Antoni

<120> Ornithine Biosynthesis Enzymes

<130> BB-1174

<140> 09/744,100
<141> 2001-01-16

<150> PCT/US99/15931
<151> 1999-07-14

<150> 60/093,209
<151> 1998-07-17

<160> 12

<170> Microsoft Office 97

B4

<210> 1
<211> 1201
<212> DNA
<213> Zea mays

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tgcaagcccc cttgccgccc ctacttgccg tcgcagccgc ctccgcatct ccgccacatc 180
cacggctgcg ccgtctcctt cgtcggctgc cgctgccacc gcgtcgctga tcgagtgga 240
cgtgctctcg gaggcgctcc cttttattca gcgattcaaa ggcaagacgg tggtggtcaa 300
gtacggcggt gcggcgatga agtccccgga gctgcaggcg tccgtgatcc gcgatctcgt 360
gctgctctcc tgcgtcggcc tccgccccgt gcttgttcac ggcggcggtc cggagattaa 420
ttcctggctg ctgcgcgtcg gcgtcgagcc gcagttccgc gacggcctcc gcgtcacgga 480
cgcgctcacc atggaggtcg tcgagatggt gctagtcggg aaggtcaaca aaaaccttgt 540
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tatcaccgct cgcccgtctc caaatgcagc ggcgctggga ttcgtcggcg aggtttcgcg 660
cgtggacgcc accgtcctcc atcccatcat cgccgcgggc catatcccgg ttatcgccac 720
cgttgccgcc gacgagactg ggcaagccta taacatcaat gctgatacgg cggctggcga 780
gattgccgct gccgtgggcg ccgagaagct gctgttgctc acagatgtgt ctggcatttt 840
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gatggtggct gacgggaagg tagctggtgg gatgataccc aaggtggagt gttgtgttca 960
cgcccttgca caaggtgtac acaccgcaag tatcattgat gggcgtgttc cacactctct 1020
tctgcttgag attctcacag acgagggcac aggcaccatg atcactggct gagctgcttc 1080
atgccttcat ggtattttcc tgtgcctctt ttctcatatt gttgtgtttt atggctatgt 1140
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<210> 2
<211> 345
<212> PRT
<213> Zea mays

<400> 2
Met Leu Leu Thr Lys Pro Tyr Leu Ser Asn Ser Leu Leu Pro Val Pro

```
Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro
            20              25                  30
```

```
Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr
        35              40                  45
```

```
Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Ala Thr Ala Ser
    50              55                  60
```

```
Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg
65              70                  75                      80
```

```
Phe Lys Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys
                85                  90                  95
```

```
Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser
            100             105             110
```

```
Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
        115             120             125
```

```
Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly
    130             135             140
```

```
Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu
145             150             155                     160
```

```
Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly
                165             170             175
```

```
Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala
            180             185             190
```

```
Arg Pro Ser Pro Asn Ala Ala Ala Leu Gly Phe Val Gly Glu Val Ser
        195             200             205
```

```
Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile
    210             215             220
```

```
Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn
225             230             235                     240
```

```
Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala
            245             250             255
```

```
Glu Lys Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg
            260             265             270
```

```
Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg
        275             280             285
```

```
Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val
    290             295             300
```

```
Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile
305             310             315                     320
```

```
Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
```

2

Glu Gly Thr Gly Thr Met Ile Thr Gly
          340   345

<210> 3
<211> 1186
<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (613)
<223> n = A, C, G, or T

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catcgccgcc tctcccgccc ctcgacgctg cctccgtctc gccgtcacat ccgccgcggc   180
gccggctgct tcgtcggcgg aggcggcggc ggcgctgagc cgcgtggatg tgctctcaga   240
ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc   300
ggcgatgaag tcgccggagc tccaggcttc agtgatccgc gacctggtcc tcctctcgtg   360
cgtcggcctc accccgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct   420
ccgcgtcggc gtcgagccgc agttccggaa cggcctccgc gtcactgacg cgctcaacat   480
ggaggtcgtc gagatggtgc tcgtccgcaa ggtcaacaaa gaactcctct ccctcatcaa   540
actcccgggg gggagcgccg taagtctctg ttggaaggaa gctcgcctcc tcaacgagcg   600
gccctccccg aangaaaagg gccttcggtt tgtcggcggg gtctggcgcg tggacgccac   660
cgtcctccac ccaatcatcg cctccggtca catcccggtc atcgccactg tgggcgccga   720
cgagaccggg caggcctaca acatcaacgc tgacacggcg gccggcgaga tcgccgccgc   780
ggtcggcgcg gagaagctgt tgctgctcac agatgtgtct ggaattctgg ccgaccgtaa   840
tgaccccggg agtctggtga aagagatcga cattgctggg gtgcggcaga tggtggccga   900
cgggcaggta gctggtggga tgataccgaa ggtggaatgc tgcgtgcgtg ccctcgcaca   960
gggcgtgcac actgcaagca tcatcgatgg gcgtgtcccg cactcgttgc tgctcgagat 1020
tctcacagat gagggcactg gcactatgat cactggctga ggtgattcat cccgtcgtgg 1080
tattctccgg tgcctctctt ctcatactgt aatgtaattt gcatttgata tgcctcatga 1140
ttgcaataag aattgtattc ctcaaaaaaa aaaaaaaaa aaaaaa   1186

<210> 4
<211> 343
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (195)
<223> Xaa = ANY AMINO ACID

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Met Leu Leu Ala Lys Pro His Leu Ser Ser Ser Ser Phe Leu Pro Ser
  1   5   10   15

Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
           20   25   30

Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
       35   40   45

Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Ala Leu Ser
      50   55   60

```
Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
65              70              75              80

Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
            85              90              95

Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
        100             105             110

Gly Leu His Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser
        115             120             125

Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
    130             135             140

Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
145             150             155             160

Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
            165             170             175

Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
        180             185             190

Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
        195             200             205

Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
    210             215             220

Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
225             230             235             240

Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys
            245             250             255

Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
        260             265             270

Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
        275             280             285

Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
    290             295             300

Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
305             310             315             320

Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly
            325             330             335

Thr Gly Thr Met Ile Thr Gly
            340

<210> 5
<211> 1204
<212> DNA
<213> Glycine max

<400> 5
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4

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ccaccgcgcc atttccgcgg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc   180
caccgagggt cagtaccgag tcgatgtgct ctcggagtcg ctccccttca tccagaaatt   240
ccgcggcaaa accatcgtcg tcaagtacgg cggcgccgcc atgaagtccc cggagctcca   300
ggcctccgtg atcaacgacc ttgtcctcct ctcctgcgtc ggcctccgcc cgtcctggt   360
ccacggcggc ggccccgaga tcaactcctg gctcggccgc ctcaacatcc ccgccgtctt   420
ccgcgacggc ctccgcgtca ccgacgccga caccatggag atcgtctcca tggtcctcgt   480
cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg   540
cctctctggc atggacggcc gcctcctcac cgcccgcccc gctcccaagg ccgccgacct   600
cggctacgtc ggcgaggtcg cacgcgtcga tcccgccgtc ctccgctccc taatcgacac   660
cagccacatc cccgtcgtca cctccgtcgc cgccgatgaa tccggacagc cctacaacat   720
caacgccgac accgtcgccg agaattggc agcgtcgctc ggcgcggaga agctgattct   780
gctgaccgat gtggcgggaa ttctggaaga tcggaacgac cctgacagct tggtgaagaa   840
gattgacata aaaggagtga agaaaatgat ggaagatgga aaagttggtg gtggaatgat   900
acctaaggtt aattgttgcg ttaggtcctt ggcgcaaggg gttattacag cgagtattat   960
tgatggtagg gttccgcatt ctttgttgct tgagattttg actgatgaag gtgctggaac 1020
tatgataact ggataagttt atttatttat ggtgtttgga ttttttcttt tcaatcaagc 1080
cttgagttga ggttgcattg cagcacttgt tttgttagag attggtgatt gttttttaagt 1140
gcgtgtaatg tgagagatgg ttgaattgaa ttgaatgttt cagaaaaaaa aaaaaaaaaa 1200
aaaa   1204

<210> 6
<211> 342
<212> PRT
<213> Glycine max

<400> 6
Met Met Ala Gly Ala Ala Lys Thr Leu Thr Asn Leu Cys Pro Ser Phe
1   5   10   15

Pro Phe Pro Thr Lys Pró Gln Asn Gln Leu Thr Thr Ser His Ala Phe
            20   25   30

Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
        35   40   45

Ala Gln Pro Pro Leu Ala Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
    50   55   60

Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
65   70   75   80

Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
                85   90   95

Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
            100   105   110

Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
        115   120   125

Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
        130   135   140

Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
145   150   155   160

Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
                165   170   175

5

```
Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
        180                 185             190

Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Glu Val Ala Arg Val Asp
        195                 200             205

Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
        210                 215             220

Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
225                 230                 235             240

Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
        245                 250                 255

Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
        260                 265                 270

Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
        275                 280                 285

Glu Asp Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Asn Cys Cys
        290                 295                 300

Val Arg Ser Leu Ala Gln Gly Val Ile Thr Ala Ser Ile Ile Asp Gly
305                 310                 315                 320

Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Ala
                325                 330                 335

Gly Thr Met Ile Thr Gly
                340
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<210> 7
<211> 1246
<212> DNA
<213> Triticum aestivum

<220>
<221> unsure
<222> (492)..(542)
<223> n = A, C, G, or T

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ctaacctaaa ggccgcccgc gtcaggcccc tcgcctcctc cgcgccccat ggacgccgcg   180
ggctccgcgt ctcggcctcc tcctcctccc tggcgccagc gcaggccgcg tccgcggcgc   240
tgaaccgcgt ggacgtcctg tcggaggcgc tccccttcat ccagcggttc aagggcaaga   300
cggtggtggt caagtacggc ggcgcggcca tgaagtcgcc ggagctgcag gcgtcggtga   360
tccgcgacct ggtcctcctc tcctgcgtcg gcctgcgccc cgtgctcgtg cacggcggcg   420
gcccggagat caactcctgg ctgcagcgcg tcggggtcta ccgcagttc cgcaacggcc   480
tccgcgtcac gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn   540
nnaagcagct cttatcccta atcaggcctg cggggaccac agcagttggc ctctgcagaa   600
aggacgggcg catcctaacg gagcgcccct ccccagacgc cgcagccctc gggttcgtcg   660
gcgaggtcac gagaaaaaac ccctctgtgc tccacccgat catcgcctcc agccacatcc   720
cggtcatcgc caccgtggct gccgacgaga ccgggcaagc ctataacatc aacgctgaca   780
ctgcggcggg ggagatcgcg ctgccattg gcgccgagaa gctgttgctg atcactgacg   840
tgtccggcat actcgcggac cgggatgacc ccgggagcct ggtgaaggag attgacatcg   900
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6

```
ccggcgtacg gcggatggtg gccgagggca aggtgggtgg gggcatgata cccaaggtgg   960
ggtgctgcgt gcgcgcgctg cgcagggcg tgcacacggc cagcatcatt gacggccgcg  1020
tcccgcactc tctcctgctc gaaatcctca ccgacgaggg caccggcacc atgatcaccg  1080
gctgaaactt gtttgtttgt tgttgttttt ttcttttctt ttttggttca cattctttgg  1140
gttggatggt tttgcatccc tcatttgtgt taaatgtgtt ttcgattcga atcctgaaca  1200
aggagtggtg aaagattgca gctttaagca aaaaaaaaa aaaaaa            1246
```

<210> 8
<211> 340
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (133)
<223> Xaa = ANY AMINO ACID

<220>
<221> UNSURE
<222> (144)..(160)
<223> Xaa = ANY AMINO ACID

<400> 8
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 1               5                  10                  15

Leu Pro Asn Pro Asn Leu Lys Ala Ala Arg Val Arg Pro Leu Ala Ser
                20           .      25                  30

Ser Ala Pro His Gly Arg Arg Gly Leu Arg Val Ser Ala Ser Ser Ser
            35                  40                  45

Ser Leu Ala Pro Ala Gln Ala Ala Ser Ala Ala Leu Asn Arg Val Asp
    50                  55                  60

Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys Gly Lys Thr
65                  70                  75                  80

Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu Leu Gln
                85                  90                  95

Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val Gly Leu Arg
            100                 105                 110

Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp Leu Gln
            115                 120                 125

Arg Val Gly Val Xaa Pro Gln Phe Arg Asn Gly Leu Arg Val Thr Xaa
    130                 135                 140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145                 150                 155                 160

Lys Gln Leu Leu Ser Leu Ile Arg Pro Ala Gly Thr Thr Ala Val Gly
            165                 170                 175

Leu Cys Arg Lys Asp Gly Arg Ile Leu Thr Glu Arg Pro Ser Pro Asp
            180                 185                 190

Ala Ala Ala Leu Gly Phe Val Gly Glu Val Thr Arg Lys Asn Pro Ser
```

```
              195                    200                    205
     Val Leu His Pro Ile Ile Ala Ser Ser His Ile Pro Val Ile Ala Thr
         210                    215                    220

     Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn Ala Asp Thr
     225                    230                    235                    240

     Ala Ala Gly Glu Ile Ala Ala Ala Ile Gly Ala Glu Lys Leu Leu Leu
                    245                    250                    255

     Ile Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asp Asp Pro Gly Ser
                    260                    265                    270

     Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Arg Met Val Ala Glu
                275                    280                    285

     Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Gly Cys Cys Val Arg
             290                    295                    300

     Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
     305                    310                    315                    320

     Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
                    325                    330                    335

     Met Ile Thr Gly
                340
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β4

```
<210> 9
<211> 439
<212> DNA
<213> Triticum aestivum

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ggggtgcggc agatggtatc cggtgggcag gttgctggtg aatgatccc aaaggtggag 180
tgctgcgtga gagccctcgc ccagggtgtg cacactgcaa gcatcatcga tgggcgtgtc 240
ccgcactcgc tgttgctcga gattctcaca gatgagggca ctggcacaat gatcaccggc 300
taaggtgtaa aatgcctcct tggtacttcc ttatgccttt ctgttcatac tgccaatctg 360
ccatgtaatt tatgccaatg tagcctcacc tcatgattgc aataagagta ccttcctgac 420
aaaaaaaaaa aaaaaaaaa                                              439
```

```
<210> 10
<211> 100
<212> PRT
<213> Triticum aestivum

<400> 10
     Ala Arg Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys Leu Leu Leu
       1                    5                    10                    15

     Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp Pro Gly Ser
                    20                    25                    30

     Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met Val Ser Gly
                35                    40                    45

     Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys Cys Val Arg
```

8

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
 65   70   75   80

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
                    85   90   95

Met Ile Thr Gly
            100

<210> 11
<211> 297
<212> PRT
<213> Synechocystis sp.

<400> 11
Met Ser Ser Thr Gln Asp Tyr Ile Gly Glu Glu Ala Ala Thr Arg Val
  1   5   10   15

Lys Ile Leu Ser Glu Ala Leu Pro Tyr Ile Gln His Phe Ala Gly Arg
                20   25   30

Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Asp Ser Asn Leu
            35   40   45

Lys Asp Lys Val Ile Arg Asp Ile Val Phe Met Ala Ser Val Gly Ile
     50   55   60

Arg Pro Val Val Val His Gly Gly Gly Pro Glu Ile Asn Thr Trp Leu
 65   70   75   80

Asp Lys Val Gly Ile Glu Pro Gln Phe Lys Asp Gly Leu Arg Val Thr
                85   90   95

Asp Ala Ala Thr Met Asp Ile Val Glu Met Val Leu Val Gly Arg Val
            100   105   110

Asn Lys Glu Leu Val Asn Leu Ile Asn Gln Ala Gly Gly Lys Ala Val
        115   120   125

Gly Leu Cys Gly Lys Asp Gly Gln Leu Met Thr Ala Arg Thr Met Thr
    130   135   140

Asn Lys Asp Val Gly Phe Val Gly Glu Val Ser Ser Val Asp Ala Arg
145   150   155   160

Val Val Glu Thr Leu Val Lys Ser Gly Tyr Ile Pro Val Ile Ser Ser
                165   170   175

Val Ala Ala Asp Glu Phe Gly Gln Ala His Asn Ile Asn Ala Asp Thr
            180   185   190

Cys Ala Gly Glu Leu Ala Ala Ala Leu Gly Ala Glu Lys Leu Ile Leu
        195   200   205

Leu Thr Asp Thr Arg Gly Ile Leu Arg Asp Tyr Lys Asp Pro Ser Thr
    210   215   220

Leu Ile His Lys Leu Asp Ile Gln Gln Ala Arg Glu Leu Ile Gly Ser

9

```
        225                    230                         235                          240

Gly Ile Val Ala Gly Gly Met Ile Pro Lys Val Thr Cys Cys Val Arg
                245                 250                 255


Ser Leu Ala Gln Gly Val Arg Ala Ala His Ile Leu Asp Gly Arg Leu
                260                 265                 270


Pro His Ala Leu Leu Leu Glu Val Phe Thr Asp Leu Gly Ile Gly Ser
        275                 280                 285


Met Ile Val Ala Ser Gly Tyr Asp Leu
    290                 295
```

<210> 12
<211> 346
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CONSENSUS

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<221> UNSURE
<222> (2)
<223> Xaa = Leu OR Met

<220>
<221> UNSURE
<222> (3)
<223> Xaa = Leu OR Ala

<220>
<221> UNSURE
<222> (4)
<223> Xaa = Thr, Ala, OR Gly

<220>
<221> UNSURE
<222> (5)
<223> Xaa = Lys OR NONE

<220>
<221> UNSURE
<222> (6)
<223> Xaa = Pro OR NONE

<220>
<221> UNSURE
<222> (7)
<223> Xaa = His, Tyr, OR NONE

<220>
<221> UNSURE
<222> (8)
<223> Xaa = Leu OR NONE

<220>
<221> UNSURE

10
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<222> (9)
<223> Xaa = Ser, Ala, OR NONE

<220>
<221> UNSURE
<222> (10)
<223> Xaa = Asn, Ser, Ala, OR NONE

<220>
<221> UNSURE
<222> (11)
<223> Xaa = Ser, Lys, OR Pro

<220>
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<222> (12)
<223> Xaa = Leu, Ser, Thr, OR Ala

<220>
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<222> (13)
<223> Xaa = Leu OR Phe

<220>
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<222> (14)
<223> Xaa = Pro, Thr, OR NONE

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<223> Xaa = Val, Leu, OR Asn

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<222> (16)
<223> Xaa = Pro OR Leu

<220>
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<222> (17)
<223> Xaa = Ser OR Cys

<220>
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<222> (18)
<223> Xaa = Pro, Thr, OR Ala

<220>
<221> UNSURE
<222> (19)
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11

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B4

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β4

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β4

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B4

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β4

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β4

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B4

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B4

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Xaa Phe Xaa Gly Lys Thr Xaa Val Val Lys Tyr Gly Gly Ala Ala Met
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Lys Ser Pro Glu Leu Gln Ala Ser Val Ile Xaa Asp Leu Val Leu Leu
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22

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Ile Asn Ser Trp Leu Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Phe Arg Xaa
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Gly Leu Arg Val Thr Asp Ala Xaa Xaa Met Glu Xaa Val Xaa Met Val
145             150             155                     160

Leu Val Xaa Lys Val Asn Lys Xaa Leu Xaa Ser Leu Ile Xaa Xaa Xaa
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Gly Xaa Xaa Ala Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Arg Leu Xaa Xaa
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Xaa Arg Pro Xaa Pro Xaa Xaa Xaa Xaa Leu Xaa Xaa Val Gly Xaa Val
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Xaa Arg Xaa Xaa Xaa Xaa Val Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa His
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Ile Pro Val Xaa Xaa Xaa Val Xaa Ala Asp Glu Xaa Gly Gln Xaa Tyr
225             230             235                     240

Asn Ile Asn Ala Asp Thr Xaa Ala Gly Glu Xaa Ala Ala Xaa Xaa Gly
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Ala Glu Lys Leu Xaa Leu Xaa Thr Asp Val Xaa Gly Ile Leu Xaa Asp
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Arg Xaa Asp Pro Xaa Ser Leu Val Lys Xaa Xaa Asp Ile Xaa Gly Val
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Arg Xaa Met Xaa Xaa Xaa Gly Xaa Val Xaa Gly Gly Met Ile Pro Lys
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Val Xaa Cys Cys Val Xaa Xaa Leu Ala Gln Gly Val Xaa Thr Ala Ser
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Ile Leu Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr
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Asp Glu Gly Xaa Gly Thr Met Ile Thr Gly
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